

DRAFT

Figure 2. The phylogeny of the Acipenseridae type standard sequences based on maximum parsimony analysis of 76 total variable sites from the 270 bp target region of cytochrome *b*. Numbers at the nodes indicate the proportion of 500 bootstrap resamplings that support the respective species groupings. Type samples are identified as the following: AbaG11324 (*Acipenser baerii*), AbaG41168 (*Acipenser baerii*), AbrF10241 (*Acipenser brevirostrum*), AfuE40805 (*Acipenser fulvescens*), AguG20874 (*Acipenser gueldenstaedtii*), AguG20923 (*Acipenser gueldenstaedtii*), AmeF10704 (*Acipenser medirostris*), AnuG41203 (*Acipenser nudiventris*), AoxF41302 (*Acipenser oxyrinchus*), AruG20915 (*Acipenser ruthenus*), AruG20916 (*Acipenser ruthenus*), AruG41158 (*Acipenser ruthenus*), AshF40705 (*Acipenser schrenckii*), AstG20904 (*Acipenser stellatus*), AstG20907 (*Acipenser stellatus*), AstG20909 (*Acipenser stellatus*), AtrF10246 (*Acipenser transmontanus*), HdaF40717 (*Huso dauricus*), HhuG20913 (*Huso huso*), PspD10570 (*Polyodon spathula*), PspGBM6491 (*Polyodon spathula*), SalB40622 (*Scaphirhynchus albus*), SplF11159 (*Scaphirhynchus platorhynchus*), SsuH10433 (*Scaphirhynchus suttkusi*)

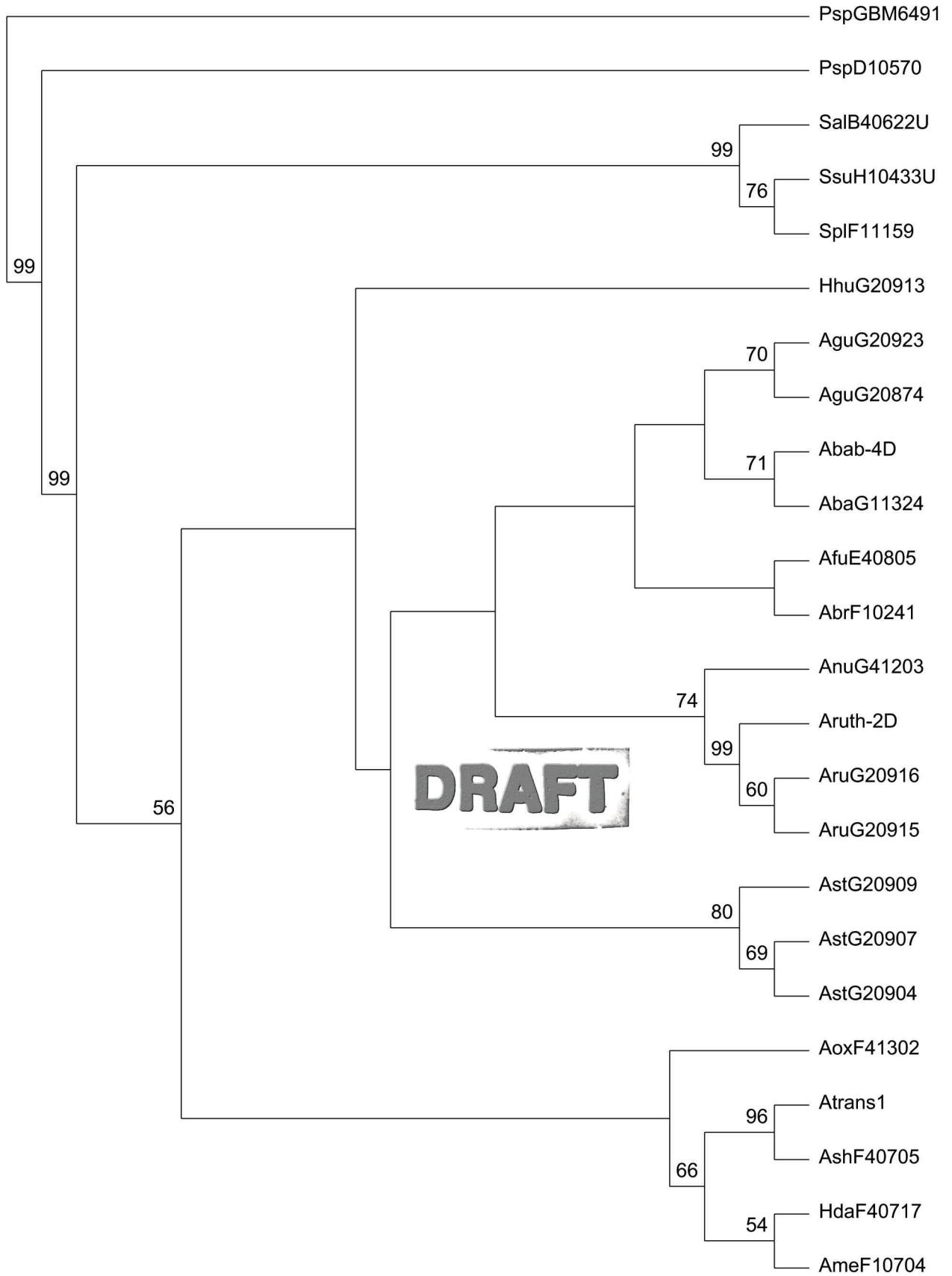


Fig. 2